



7683-031

SEQUENCE LISTING

RECEIVED

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TECH CENTER 1600/2900

(1) GENERAL INFORMATION:

(i) APPLICANT: Ullrich, Axel  
Alves, Frauke

(ii) TITLE OF INVENTION: MCK-10, A Novel Receptor Tyrosine Kinase

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Pennie & Edmonds
- (B) STREET: 1155 Avenue of the Americas
- (C) CITY: New York
- (D) STATE: New York
- (E) COUNTRY: U.S.A.
- (F) ZIP: 10036-2711

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/153,397
- (B) FILING DATE: 16-NOV-1993
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Coruzzi, Laura A.
- (B) REGISTRATION NUMBER: 30,742
- (C) REFERENCE/DOCKET NUMBER: 7683-031

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (212) 790-9090
- (B) TELEFAX: (212) 869-9741/8864
- (C) TELEX: 66141 PENNIE

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3962 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 321..3077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGGCCTGAG ACTGGGGTGA CTGGGACCTA AGAGAATCCT GAGCTGGAGG CCCCCGACAG  
60

CTGCTCTCGG GAGCCGCCCTC CCGACACCCG AGCCCCGCCG GCGCCTCCCCG CTCCCCGGCTC  
120

CCGGCTCCTG GCTCCCTCCG CCTCCCCCGC CCCTCGCCCC GCCGCCGAAG AGGCCCGCT  
180

CCCGGGTCGG ACGCCTGGGT CTGCCGGGAA GAGCGATGAG AGGTGTCTGA AGGTGGCTAT  
240

TCACTGAGCG ATGGGGTTGG ACTTGAAAGGA ATGCCAAGAG ATGCTGCCCC CACCCCCCTTA  
300

GGCCCGAGGG ATCAGGAGCT ATG GGA CCA GAG GCC CTG TCA TCT TTA CTG  
350

Met Gly Pro Glu Ala Leu Ser Ser Leu Leu  
1 5 10

CTG CTG CTC TTG GTG GCA AGT GGA GAT GCT GAC ATG AAG GGA CAT TTT  
398

Leu Leu Leu Leu Val Ala Ser Gly Asp Ala Asp Met Lys Gly His Phe  
15 20 25

GAT CCT GCC AAG TGC CGC TAT GCC CTG GGC ATG CAG GAC CGG ACC ATC  
446

Asp Pro Ala Lys Cys Arg Tyr Ala Leu Gly Met Gln Asp Arg Thr Ile  
 30 35 40

CCA GAC AGT GAC ATC TCT GCT TCC AGC TCC TGG TCA GAT TCC ACT GCC

494

Pro	Asp	Ser	Asp	Ile	Ser	Ala	Ser	Ser	Ser	Trp	Ser	Asp	Ser	Thr	Ala
45							50								55

GCC CGC CAC AGC AGG TTG GAG AGC AGT GAC GGG GAT GGG GCC TGG TGC  
542

Ala	Arg	His	Ser	Arg	Leu	Glu	Ser	Ser	Asp	Gly	Asp	Gly	Ala	Trp	Cys
60					65								70		

CCC GCA GGG TCG GTG TTT CCC AAG GAG GAG GAG TAC TTG CAG GTG GAT  
590

Pro	Ala	Gly	Ser	Val	Phe	Pro	Lys	Glu	Glu	Glu	Tyr	Leu	Gln	Val	Asp
75					80						85				90

CTA CAA CGA CTC CAC CTG GTG GCT CTG GTG GGC ACC CAG GGA CGG CAT  
638

Leu	Gln	Arg	Leu	His	Leu	Val	Ala	Leu	Val	Gly	Thr	Gln	Gly	Arg	His
95									100					105	

GCC GGG GGC CTG GGC AAG GAG TTC TCC CGG AGC TAC CGG CTG CGT TAC  
686

Ala	Gly	Gly	Leu	Gly	Lys	Glu	Phe	Ser	Arg	Ser	Tyr	Arg	Leu	Arg	Tyr
110								115					120		

TCC CGG GAT GGT CGC CGC TGG ATG GGC TGG AAG GAC CGC TGG GGT CAG  
734

Ser	Arg	Asp	Gly	Arg	Arg	Trp	Met	Gly	Trp	Lys	Asp	Arg	Trp	Gly	Gln
125							130					135			

GAG GTG ATC TCA GGC AAT GAG GAC CCT GAG GGA GTG GTG CTG AAG GAC  
782

Glu	Val	Ile	Ser	Gly	Asn	Glu	Asp	Pro	Glu	Gly	Val	Val	Leu.	Lys	Asp
140						145						150			

CTT GGG CCC CCC ATG GTT GCC CGA CTG GTT CGC TTC TAC CCC CGG GCT  
830

Leu	Gly	Pro	Pro	Met	Val	Ala	Arg	Leu	Val	Arg	Phe	Tyr	Pro	Arg	Ala
155						160				165				170	

GAC CGG GTC ATG AGT GTC TGT CTG CGG GTA GAG CTC TAT GGC TGC CTC  
878

Asp	Arg	Val	Met	Ser	Val	Cys	Leu	Arg	Val	Glu	Leu	Tyr	Gly	Cys	Leu
175									180					185	

TGG AGG GAT GGA CTC CTG TCT TAC ACC GCC CCT GTG GGG CAG ACA ATG  
926

Trp	Arg	Asp	Gly	Leu	Leu	Ser	Tyr	Thr	Ala	Pro	Val	Gly	Gln	Thr	Met
190								195					200		

TAT TTA TCT GAG GCC GTG TAC CTC AAC GAC TCC ACC TAT GAC GGA CAT  
974  
 Tyr Leu Ser Glu Ala Val Tyr Leu Asn Asp Ser Thr Tyr Asp Gly His  
205 210 215

ACC GTG GGC GGA CTG CAG TAT GGG GGT CTG GGC CAG CTG GCA GAT GGT  
1022  
 Thr Val Gly Gly Leu Gln Tyr Gly Gly Leu Gly Gln Leu Ala Asp Gly  
220 225 230

GTG GTG GGG CTG GAT GAC TTT AGG AAG AGT CAG GAG CTG CGG GTC TGG  
1070  
 Val Val Gly Leu Asp Asp Phe Arg Lys Ser Gln Glu Leu Arg Val Trp  
235 240 245 250

CCA GGC TAT GAC TAT GTG GGA TGG AGC AAC CAC AGC TTC TCC AGT GGC  
1118  
 Pro Gly Tyr Asp Tyr Val Gly Trp Ser Asn His Ser Phe Ser Ser Gly  
255 260 265

TAT GTG GAG ATG GAG TTT GAG TTT GAC CGG CTG AGG GCC TTC CAG GCT  
1166  
 Tyr Val Glu Met Glu Phe Glu Phe Asp Arg Leu Arg Ala Phe Gln Ala  
270 275 280

ATG CAG GTC CAC TGT AAC AAC ATG CAC ACG CTG GGA GCC CGT CTG CCT  
1214  
 Met Gln Val His Cys Asn Asn Met His Thr Leu Gly Ala Arg Leu Pro  
285 290 295

GGC GGG GTG GAA TGT CGC TTC CGG CGT GGC CCT GCC ATG GCC TGG GAG  
1262  
 Gly Gly Val Glu Cys Arg Phe Arg Arg Gly Pro Ala Met Ala Trp Glu  
300 305 310

GGG GAG CCC ATG CGC CAC AAC CTA GGG GGC AAC CTG GGG GAC CCC AGA  
1310  
 Gly Glu Pro Met Arg His Asn Leu Gly Gly Asn Leu Gly Asp Pro Arg  
315 320 325 330

GCC CGG GCT GTC TCA GTG CCC CTT GGC GGC CGT GTG GCT CGC TTT CTG  
1358  
 Ala Arg Ala Val Ser Val Pro Leu Gly Gly Arg Val Ala Arg Phe Leu  
335 340 345

CAG TGC CGC TTC CTC TTT GCG GGG CCC TGG TTA CTC TTC AGC GAA ATC  
1406

Gln Cys Arg Phe Leu Phe Ala Gly Pro Trp Leu Leu Phe Ser Glu Ile  
 350 355 360

TCC TTC ATC TCT GAT GTG GTG AAC AAT TCC TCT CCG GCA CTG GGA GGC  
 1454

Ser Phe Ile Ser Asp Val Val Asn Asn Ser Ser Pro Ala Leu Gly Gly  
 365 370 375

ACC TTC CCG CCA GCC CCC TGG TGG CCG CCT GGC CCA CCT CCC ACC AAC  
 1502

Thr Phe Pro Pro Ala Pro Trp Trp Pro Pro Gly Pro Pro Pro Thr Asn  
 380 385 390

TTC AGC AGC TTG GAG CTG GAG CCC AGA GGC CAG CAG CCC GTG GCC AAG  
 1550

Phe Ser Ser Leu Glu Leu Glu Pro Arg Gly Gln Gln Pro Val Ala Lys  
 395 400 405 410

GCC GAG GGG AGC CCG ACC GCC ATC CTC ATC GGC TGC CTG GTG GCC ATC  
 1598

Ala Glu Gly Ser Pro Thr Ala Ile Leu Ile Gly Cys Leu Val Ala Ile  
 415 420 425

ATC CTG CTC CTG CTG CTC ATC ATT GCC CTC ATG CTC TGG CGG CTG CAC  
 1646

Ile Leu Leu Leu Leu Ile Ile Ala Leu Met Leu Trp Arg Leu His  
 430 435 440

TGG CGC AGG CTC CTC AGC AAG GCT GAA CGG AGG GTG TTG GAA GAG GAG  
 1694

Trp Arg Arg Leu Leu Ser Lys Ala Glu Arg Arg Val Leu Glu Glu Glu  
 445 450 455

CTG ACG GTT CAC CTC TCT GTC CCT GGG GAC ACT ATC CTC ATC AAC AAC  
 1742

Leu Thr Val His Leu Ser Val Pro Gly Asp Thr Ile Leu Ile Asn Asn  
 460 465 470

CGC CCA GGT CCT AGA GAG CCA CCC CCG TAC CAG GAG CCC CGG CCT CGT  
 1790

Arg Pro Gly Pro Arg Glu Pro Pro Pro Tyr Gln Glu Pro Arg Pro Arg  
 475 480 485 490

GGG AAT CCG CCC CAC TCC GCT CCC TGT GTC CCC AAT GGC TCT GCG TTG  
 1838

Gly Asn Pro Pro His Ser Ala Pro Cys Val Pro Asn Gly Ser Ala Leu  
 495 500 505

CTG CTC TCC AAT CCA GCC TAC CGC CTC CTT CTG GCC ACT TAC GCC CGT  
 1886  
 Leu Leu Ser Asn Pro Ala Tyr Arg Leu Leu Ala Thr Tyr Ala Arg  
 510 515 520

CCC CCT CGA GGC CCG GGC CCC CCC ACA CCC GCC TGG GCC AAA CCC ACC  
 1934  
 Pro Pro Arg Gly Pro Gly Pro Pro Thr Pro Ala Trp Ala Lys Pro Thr  
 525 530 535

AAC ACC CAG GCC TAC AGT GGG GAC TAT ATG GAG CCT GAG AAG CCA GGC  
 1982  
 Asn Thr Gln Ala Tyr Ser Gly Asp Tyr Met Glu Pro Glu Lys Pro Gly  
 540 545 550

GCC CCG CTT CTG CCC CCA CCT CCC CAG AAC AGC GTC CCC CAT TAT GCC  
 2030  
 Ala Pro Leu Leu Pro Pro Pro Pro Gln Asn Ser Val Pro His Tyr Ala  
 555 560 565 570

GAG GCT GAC ATT GTT ACC CTG CAG GGC GTC ACC GGG GGC AAC ACC TAT  
 2078  
 Glu Ala Asp Ile Val Thr Leu Gln Gly Val Thr Gly Gly Asn Thr Tyr  
 575 580 585

GCT GTG CCT GCA CTG CCC CCA GGG GCA GTC GGG GAT GGG CCC CCC AGA  
 2126  
 Ala Val Pro Ala Leu Pro Pro Gly Ala Val Gly Asp Gly Pro Pro Arg  
 590 595 600

GTG GAT TTC CCT CGA TCT CGA CTC CGC TTC AAG GAG AAG CTT GGC GAG  
 2174  
 Val Asp Phe Pro Arg Ser Arg Leu Arg Phe Lys Glu Lys Leu Gly Glu  
 605 610 615

GGC CAG TTT GGG GAG GTG CAC CTG TGT GAG GTC GAC AGC CCT CAA GAT  
 2222  
 Gly Gln Phe Gly Glu Val His Leu Cys Glu Val Asp Ser Pro Gln Asp  
 620 625 630

CTG GTC AGT CTT GAT TTC CCC CTT AAT GTG CGT AAG GGA CAC CCT TTG  
 2270  
 Leu Val Ser Leu Asp Phe Pro Leu Asn Val Arg Lys Gly His Pro Leu  
 635 640 645 650

CTG GTA GCT GTC AAG ATC TTA CGG CCA GAT GCC ACC AAG AAT GCC AGC  
 2318  
 Leu Val Ala Val Lys Ile Leu Arg Pro Asp Ala Thr Lys Asn Ala Ser

655	660	665
TTC TCC TTG TTC TCC AGG AAT GAT TTC CTG AAA GAG GTG AAG ATC ATG 2366		
Phe Ser Leu Phe Ser Arg Asn Asp Phe Leu Lys Glu Val Lys Ile Met 670                       675                       680		
TCG AGG CTC AAG GAC CCC AAC ATC ATT CGG CTG CTG GGC GTG TGT GTG 2414		
Ser Arg Leu Lys Asp Pro Asn Ile Ile Arg Leu Leu Gly Val Cys Val 685                       690                       695		
CAG GAC GAC CCC CTC TGC ATG ATT ACT GAC TAC ATG GAG AAC GGC GAC 2462		
Gln Asp Asp Pro Leu Cys Met Ile Thr Asp Tyr Met Glu Asn Gly Asp 700                       705                       710		
CTC AAC CAG TTC CTC AGT GCC CAC CAG CTG GAG GAC AAG GCA GCC GAG 2510		
Leu Asn Gln Phe Leu Ser Ala His Gln Leu Glu Asp Lys Ala Ala Glu 715                       720                       725                       730		
GGG GCC CCT GGG GAC GGG CAG GCT GCG CAG GGG CCC ACC ATC AGC TAC 2558		
Gly Ala Pro Gly Asp Gly Gln Ala Ala Gln Gly Pro Thr Ile Ser Tyr 735                       740                       745		
CCA ATG CTG CTG CAT GTG GCA GCC CAG ATC GCC TCC GGC ATG CGC TAT 2606		
Pro Met Leu Leu His Val Ala Ala Gln Ile Ala Ser Gly Met Arg Tyr 750                       755                       760		
CTG GCC ACA CTC AAC TTT GTA CAT CGG GAC CTG GCC ACG CGG AAC TGC 2654		
Leu Ala Thr Leu Asn Phe Val His Arg Asp Leu Ala Thr Arg Asn Cys 765                       770                       775		
CTA GTT GGG GAA AAT TTC ACC ATC AAA ATC GCA GAC TTT GGC ATG AGC 2702		
Leu Val Gly Glu Asn Phe Thr Ile Lys Ile Ala Asp Phe Gly Met Ser 780                       785                       790		
CGG AAC CTC TAT GCT GGG GAC TAT TAC CGT GTG CAG GGC CGG GCA GTG 2750		
Arg Asn Leu Tyr Ala Gly Asp Tyr Tyr Arg Val Gln Gly Arg Ala Val 795                       800                       805                       810		
CTG CCC ATC CGC TGG ATG GCC TGG GAG TGC ATC CTC ATG GGG AAG TTC		

2798  
Leu Pro Ile Arg Trp Met Ala Trp Glu Cys Ile Leu Met Gly Lys Phe  
815 820 825

ACG ACT GCG AGT GAC GTG TGG GCC TTT GGT GTG ACC CTG TGG GAG GTG  
2846  
Thr Thr Ala Ser Asp Val Trp Ala Phe Gly Val Thr Leu Trp Glu Val  
830 835 840

CTG ATG CTC TGT AGG GCC CAG CCC TTT GGG CAG CTC ACC GAC GAG CAG  
2894  
Leu Met Leu Cys Arg Ala Gln Pro Phe Gly Gln Leu Thr Asp Glu Gln  
845 850 855

GTC ATC GAG AAC GCG GGG GAG TTC TTC CGG GAC CAG GGC CGG CAG GTG  
2942  
Val Ile Glu Asn Ala Gly Glu Phe Phe Arg Asp Gln Gly Arg Gln Val  
860 865 870

TAC CTG TCC CGG CCG CCT GCC TGC CCG CAG GGC CTA TAT GAG CTG ATG  
2990  
Tyr Leu Ser Arg Pro Pro Ala Cys Pro Gln Gly Leu Tyr Glu Leu Met  
875 880 890

CTT CGG TGC TGG AGC CGG GAG TCT GAG CAG CGA CCA CCC TTT TCC CAG  
3038  
Leu Arg Cys Trp Ser Arg Glu Ser Glu Gln Arg Pro Pro Phe Ser Gln  
895 900 905

CTG CAT CGG TTC CTG GCA GAG GAT GCA CTC AAC ACG GTG TGAATCACAC  
3087  
Leu His Arg Phe Leu Ala Glu Asp Ala Leu Asn Thr Val  
910 915

ATCCAGCTGC CCCTCCCTCA GGGAGTGATC CAGGGGAAGC CAGTGACACT AAAACAAGAG  
3147

GACACAATGG CACCTCTGCC CTTCCCTCC CGACAGCCC TCACCTCTAA TAGAGGCAGT  
3207

GAGACTGCAG GTGGGCTGGG CCCACCCAGG GAGCTGATGC CCCTTCTCCC CTTCTGGAC  
3267

ACACTCTCAT GTCCCCCTCC TGTTCTTCCT TCCTAGAACGC CCCTGTCGCC CACCCAGCTG  
3327

GTCCCTGTGGA TGGGATCCTC TCCACCCCTCC TCTAGCCATC CCTTGGGGAA GGGTGGGGAG  
3387

AAATATAGGA TAGACACTGG ACATGGCCCA TTGGAGCACC TGGGCCAAC TGGACAACAC  
3447

TGATTCTGG AGAGGTGGCT GCGCCCCAGC TTCTCTCTCC CTGTCACACA CTGGACCCCA  
3507

CTGGCTGAGA ATCTGGGGT GAGGAGGACA AGAAGGAGAG GAAAATGTTT CCTTGTGCCT  
3567

GCTCCTGTAC TTGTCCTCAG CTTGGCTTC TTCCTCCTCC ATCACCTGAA ACACGGACC  
3627

TGGGGTAGC CCCGCCAG CCCTCAGTCA CCCCCACTTC CCACTGCAG TCTTGTAGCT  
3687

AGAACTTCTC TAAGCCTATA CGTTCTGTG GAGTAAATAT TGGGATTGGG GGGAAAGAGG  
3747

GAGCAACGGC CCATAGCCTT GGGGTTGGAC ATCTCTAGTG TAGCTGCCAC ATTGATTTT  
3807

CTATAATCAC TTGGGGTTTG TACATTTTG GGGGGAGAGA CACAGATTTT TACACTAATA  
3867

TATGGACCTA GCTTGAGGCA ATTTAATCC CCTGCACTAG GCAGGTAATA ATAAAGGTTG  
3927

AGTTTCCAC AAAAAAAA AAAAAACCGG AATTC  
3962

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 919 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Pro Glu Ala Leu Ser Ser Leu Leu Leu Leu Leu Val Ala  
1 5 10 15

Ser Gly Asp Ala Asp Met Lys Gly His Phe Asp Pro Ala Lys Cys Arg  
20 25 30

Tyr Ala Leu Gly Met Gln Asp Arg Thr Ile Pro Asp Ser Asp Ile Ser  
           35                        40                                45

Ala Ser Ser Ser Trp Ser Asp Ser Thr Ala Ala Arg His Ser Arg Leu  
       50                            55                                60

Glu Ser Ser Asp Gly Asp Gly Ala Trp Cys Pro Ala Gly Ser Val Phe  
       65                            70                                75                            80

Pro Lys Glu Glu Glu Tyr Leu Gln Val Asp Leu Gln Arg Leu His Leu  
       85                            90                                95

Val Ala Leu Val Gly Thr Gln Gly Arg His Ala Gly Gly Leu Gly Lys  
       100                           105                                110

Glu Phe Ser Arg Ser Tyr Arg Leu Arg Tyr Ser Arg Asp Gly Arg Arg  
       115                           120                                125

Trp Met Gly Trp Lys Asp Arg Trp Gly Gln Glu Val Ile Ser Gly Asn  
       130                           135                                140

Glu Asp Pro Glu Gly Val Val Leu Lys Asp Leu Gly Pro Pro Met Val  
       145                           150                                155                            160

Ala Arg Leu Val Arg Phe Tyr Pro Arg Ala Asp Arg Val Met Ser Val  
       165                           170                                175

Cys Leu Arg Val Glu Leu Tyr Gly Cys Leu Trp Arg Asp Gly Leu Leu  
       180                           185                                190

Ser Tyr Thr Ala Pro Val Gly Gln Thr Met Tyr Leu Ser Glu Ala Val  
       195                           200                                205

Tyr Leu Asn Asp Ser Thr Tyr Asp Gly His Thr Val Gly Gly Leu Gln  
       210                           215                                220

Tyr Gly Gly Leu Gly Gln Leu Ala Asp Gly Val Val Gly Leu Asp Asp  
       225                           230                                235                            240

Phe Arg Lys Ser Gln Glu Leu Arg Val Trp Pro Gly Tyr Asp Tyr Val  
       245                           250                                255

Gly Trp Ser Asn His Ser Phe Ser Ser Gly Tyr Val Glu Met Glu Phe  
       260                           265                                270

Glu Phe Asp Arg Leu Arg Ala Phe Gln Ala Met Gln Val His Cys Asn  
       275                           280                                285

Asn Met His Thr Leu Gly Ala Arg Leu Pro Gly Gly Val Glu Cys Arg  
 290 295 300  
 Phe Arg Arg Gly Pro Ala Met Ala Trp Glu Gly Glu Pro Met Arg His  
 305 310 315 320  
 Asn Leu Gly Gly Asn Leu Gly Asp Pro Arg Ala Arg Ala Val Ser Val  
 325 330 335  
 Pro Leu Gly Gly Arg Val Ala Arg Phe Leu Gln Cys Arg Phe Leu Phe  
 340 345 350  
 Ala Gly Pro Trp Leu Leu Phe Ser Glu Ile Ser Phe Ile Ser Asp Val  
 355 360 365  
 Val Asn Asn Ser Ser Pro Ala Leu Gly Gly Thr Phe Pro Pro Ala Pro  
 370 375 380  
 Trp Trp Pro Pro Gly Pro Pro Pro Thr Asn Phe Ser Ser Leu Glu Leu  
 385 390 395 400  
 Glu Pro Arg Gly Gln Gln Pro Val Ala Lys Ala Glu Gly Ser Pro Thr  
 405 410 415  
 Ala Ile Leu Ile Gly Cys Leu Val Ala Ile Ile Leu Leu Leu Leu  
 420 425 430  
 Ile Ile Ala Leu Met Leu Trp Arg Leu His Trp Arg Arg Leu Leu Ser  
 435 440 445  
 Lys Ala Glu Arg Arg Val Leu Glu Glu Leu Thr Val His Leu Ser  
 450 455 460  
 Val Pro Gly Asp Thr Ile Leu Ile Asn Asn Arg Pro Gly Pro Arg Glu  
 465 470 475 480  
 Pro Pro Pro Tyr Gln Glu Pro Arg Pro Arg Gly Asn Pro Pro His Ser  
 485 490 495  
 Ala Pro Cys Val Pro Asn Gly Ser Ala Leu Leu Leu Ser Asn Pro Ala  
 500 505 510  
 Tyr Arg Leu Leu Leu Ala Thr Tyr Ala Arg Pro Pro Arg Gly Pro Gly  
 515 520 525  
 Pro Pro Thr Pro Ala Trp Ala Lys Pro Thr Asn Thr Gln Ala Tyr Ser  
 530 535 540

Gly Asp Tyr Met Glu Pro Glu Lys Pro Gly Ala Pro Leu Leu Pro Pro  
 545 550 555 560

Pro Pro Gln Asn Ser Val Pro His Tyr Ala Glu Ala Asp Ile Val Thr  
 565 570 575

Leu Gln Gly Val Thr Gly Gly Asn Thr Tyr Ala Val Pro Ala Leu Pro  
 580 585 590

Pro Gly Ala Val Gly Asp Gly Pro Pro Arg Val Asp Phe Pro Arg Ser  
 595 600 605

Arg Leu Arg Phe Lys Glu Lys Leu Gly Glu Gly Gln Phe Gly Glu Val  
 610 615 620

His Leu Cys Glu Val Asp Ser Pro Gln Asp Leu Val Ser Leu Asp Phe  
 625 630 635 640

Pro Leu Asn Val Arg Lys Gly His Pro Leu Leu Val Ala Val Lys Ile  
 645 650 655

Leu Arg Pro Asp Ala Thr Lys Asn Ala Ser Phe Ser Leu Phe Ser Arg  
 660 665 670

Asn Asp Phe Leu Lys Glu Val Lys Ile Met Ser Arg Leu Lys Asp Pro  
 675 680 685

Asn Ile Ile Arg Leu Leu Gly Val Cys Val Gln Asp Asp Pro Leu Cys  
 690 695 700

Met Ile Thr Asp Tyr Met Glu Asn Gly Asp Leu Asn Gln Phe Leu Ser  
 705 710 715 720

Ala His Gln Leu Glu Asp Lys Ala Ala Glu Gly Ala Pro Gly Asp Gly  
 725 730 735

Gln Ala Ala Gln Gly Pro Thr Ile Ser Tyr Pro Met Leu Leu His Val  
 740 745 750

Ala Ala Gln Ile Ala Ser Gly Met Arg Tyr Leu Ala Thr Leu Asn Phe  
 755 760 765

Val His Arg Asp Leu Ala Thr Arg Asn Cys Leu Val Gly Glu Asn Phe  
 770 775 780

Thr Ile Lys Ile Ala Asp Phe Gly Met Ser Arg Asn Leu Tyr Ala Gly  
 785 790 795 800

Asp Tyr Tyr Arg Val Gln Gly Arg Ala Val Leu Pro Ile Arg Trp Met  
 805 810 815

Ala Trp Glu Cys Ile Leu Met Gly Lys Phe Thr Thr Ala Ser Asp Val  
 820 825 830

Trp Ala Phe Gly Val Thr Leu Trp Glu Val Leu Met Leu Cys Arg Ala  
 835 840 845

Gln Pro Phe Gly Gln Leu Thr Asp Glu Gln Val Ile Glu Asn Ala Gly  
 850 855 860

Glu Phe Phe Arg Asp Gln Gly Arg Gln Val Tyr Leu Ser Arg Pro Pro  
 865 870 875 880

Ala Cys Pro Gln Gly Leu Tyr Glu Leu Met Leu Arg Cys Trp Ser Arg  
 885 890 895

Glu Ser Glu Gln Arg Pro Pro Phe Ser Gln Leu His Arg Phe Leu Ala  
 900 905 910

Glu Asp Ala Leu Asn Thr Val  
 915

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3157 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 370..2934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCACGAGCGGG CACGAGTCCA TGATCTCTTT CCATCCTCCC TTTCCGTGTT GCTCACTTCT

60

TTTCTTGCTC ATCTTGAGA CTGTGCAATC CCAGATTAAC TACAAACAGA GAAGAGCTGG  
120

TGATAGCTCC AGAGCTCAGA GAAAGGAGGT CTCTTACAA GAAGTCTGGC TCTCAAAGCC  
180

TCCATCAAGG GAGACCTACA AGTTGCCTGG GGTCAGTGC TCTAGAAAGT TCCAAGGTTT  
240

GTGGCTTGAA TTATTCTAAA GAAGCTGAAA TAATTGAAGA GAAGCAGAGG CCAGCTGTTT  
300

TTGAGGATCC TGCTCCACAG AGAATGCTCT GCACCCGTTG ATACTCCAGT TCCAACACCCA  
360

TCTTCTGAG ATG ATC CTG ATT CCC AGA ATG CTC TTG GTG CTG TTC CTG  
408

Met	Ile	Leu	Ile	Pro	Arg	Met	Leu	Leu	Val	Leu	Phe	Leu
1						5						10

CTG CTG CCT ATC TTG AGT TCT GCA AAA GCT CAG GTT AAT CCA GCT ATA  
456

Leu	Leu	Pro	Ile	Leu	Ser	Ser	Ala	Lys	Ala	Gln	Val	Asn	Pro	Ala	Ile
15					20							25			

TGC CGC TAT CCT CTG GGC ATG TCA GGA GGC CAG ATT CCA GAT GAG GAC  
504

Cys	Arg	Tyr	Pro	Leu	Gly	Met	Ser	Gly	Gly	Gln	Ile	Pro	Asp	Glu	Asp
30						35				40					45

ATC ACA GCT TCC AGT CAG TGG TCA GAG TCC ACA GCT GCC AAA TAT GGA  
552

Ile	Thr	Ala	Ser	Ser	Gln	Trp	Ser	Glu	Ser	Thr	Ala	Ala	Lys	Tyr	Gly
					50				55				60		

AGG CTG GAC TCA GAA GAA GGG GAT GGA GCC TGG TGC CCT GAG ATT CCA  
600

Arg	Leu	Asp	Ser	Glu	Glu	Gly	Asp	Gly	Ala	Trp	Cys	Pro	Glu	Ile	Pro
							65		70				75		

GTG GAA CCT GAT GAC CTG AAG GAG TTT CTG CAG ATT GAC TTG CAC ACC  
648

Val	Glu	Pro	Asp	Asp	Leu	Lys	Glu	Phe	Leu	Gln	Ile	Asp	Leu	His	Thr
							80		85				90		

CTC CAT TTT ATC ACT CTG GTG GGG ACC CAG GGG CGC CAT GCA GGA GGT

696  
 Leu His Phe Ile Thr Leu Val Gly Thr Gln Gly Arg His Ala Gly Gly  
 95 100 105  
  
 CAT GGC ATC GAG TTT GCC CCC ATG TAC AAG ATC AAT TAC AGT CGG GAT  
 744  
 His Gly Ile Glu Phe Ala Pro Met Tyr Lys Ile Asn Tyr Ser Arg Asp  
 110 115 120 125  
  
 GGC ACT CGC TGG ATC TCT TGG CGG AAC CGT CAT GGG AAA CAG GTG CTG  
 792  
 Gly Thr Arg Trp Ile Ser Trp Arg Asn Arg His Gly Lys Gln Val Leu  
 130 135 140  
  
 GAT GGA AAT AGT AAC CCC TAT GAC ATT TTC CTA AAG GAC TTG GAG CCG  
 840  
 Asp Gly Asn Ser Asn Pro Tyr Asp Ile Phe Leu Lys Asp Leu Glu Pro  
 145 150 155  
  
 CCC ATT GTA GCC AGA TTT GTC CGG TTC ATT CCA GTC ACC GAC CAC TCC  
 888  
 Pro Ile Val Ala Arg Phe Val Arg Phe Ile Pro Val Thr Asp His Ser  
 160 165 170  
  
 ATG AAT GTG TGT ATG AGA GTG GAG CTT TAC GGC TGT GTC TGG CTA GAT  
 936  
 Met Asn Val Cys Met Arg Val Glu Leu Tyr Gly Cys Val Trp Leu Asp  
 175 180 185  
  
 GGC TTG GTG TCT TAC AAT GCT CCA GCT GGG CAG CAG TTT GTA CTC CCT  
 984  
 Gly Leu Val Ser Tyr Asn Ala Pro Ala Gly Gln Gln Phe Val Leu Pro  
 190 195 200 205  
  
 GGA GGT TCC ATC ATT TAT CTG AAT GAT TCT GTC TAT GAT GGA GCT GTT  
 1032  
 Gly Gly Ser Ile Ile Tyr Leu Asn Asp Ser Val Tyr Asp Gly Ala Val  
 210 215 220  
  
 GGA TAC AGC ATG ACA GAA GGG CTA GGC CAA TTG ACC GAT GGT GTG TCT  
 1080  
 Gly Tyr Ser Met Thr Glu Gly Leu Gly Gln Leu Thr Asp Gly Val Ser  
 225 230 235  
  
 GGC CTG GAC GAT TTC ACC CAG ACC CAT GAA TAC CAC GTG TGG CCC GGC  
 1128  
 Gly Leu Asp Asp Phe Thr Gln Thr His Glu Tyr His Val Trp Pro Gly  
 240 245 250

TAT GAC TAT GTG GGC TGG CGG AAC GAG AGT GCC ACC AAT GGC TAC ATT  
   1176  
 Tyr Asp Tyr Val Gly Trp Arg Asn Glu Ser Ala Thr Asn Gly Tyr Ile  
   255                         260                         265  
  
 GAG ATC ATG TTT GAA TTT GAC CGC ATC AGG AAT TTC ACT ACC ATG AAG  
   1224  
 Glu Ile Met Phe Glu Phe Asp Arg Ile Arg Asn Phe Thr Thr Met Lys  
   270                         275                         280                         285  
  
 GTC CAC TGC AAC AAC ATG TTT GCT AAA GGT GTG AAG ATC TTT AAG GAG  
   1272  
 Val His Cys Asn Asn Met Phe Ala Lys Gly Val Lys Ile Phe Lys Glu  
   290                         295                         300  
  
 GTA CAG TGC TAC TTC CGC TCT GAA GCC AGT GAG TGG GAA CCT AAT GCC  
   1320  
 Val Gln Cys Tyr Phe Arg Ser Glu Ala Ser Glu Trp Glu Pro Asn Ala  
   305                         310                         315  
  
 ATT TCC TTC CCC CTT GTC CTG GAT GAC GTC AAC CCC AGT GCT CGG TTT  
   1368  
 Ile Ser Phe Pro Leu Val Leu Asp Asp Val Asn Pro Ser Ala Arg Phe  
   320                         325                         330  
  
 GTC ACG GTG CCT CTC CAC CAC CGA ATG GCC AGT GCC ATC AAG TGT CAA  
   1416  
 Val Thr Val Pro Leu His His Arg Met Ala Ser Ala Ile Lys Cys Gln  
   335                         340                         345  
  
 TAC CAT TTT GCA GAT ACC TGG ATG ATG TTC AGT GAG ATC ACC TTC CAA  
   1464  
 Tyr His Phe Ala Asp Thr Trp Met Met Phe Ser Glu Ile Thr Phe Gln  
   350                         355                         360                         365  
  
 TCA GAT GCT GCA ATG TAC AAC AAC TCT GAA GCC CTG CCC ACC TCT CCT  
   1512  
 Ser Asp Ala Ala Met Tyr Asn Asn Ser Glu Ala Leu Pro Thr Ser Pro  
   370                         375                         380  
  
 ATG GCA CCC ACA ACC TAT GAT CCA ATG CTT AAA GTT GAT GAC AGC AAC  
   1560  
 Met Ala Pro Thr Thr Tyr Asp Pro Met Leu Lys Val Asp Asp Ser Asn  
   385                         390                         395  
  
 ACT CGG ATC CTG ATT GGC TGC TTG GTG GCC ATC ATC TTT ATC CTC CTG  
   1608

Thr Arg Ile Leu Ile Gly Cys Leu Val Ala Ile Ile Phe Ile Leu Leu  
 400 405 410

GCC ATC ATT GTC ATC ATC CTC TGG AGG CAG TTC TGG CAG AAA ATG CTG  
 1656

Ala Ile Ile Val Ile Ile Leu Trp Arg Gln Phe Trp Gln Lys Met Leu  
 415 420 425

GAG AAG GCT TCT CGG AGG ATG CTG GAT GAA ATG ACA GTC AGC CTT  
 1704

Glu Lys Ala Ser Arg Arg Met Leu Asp Asp Glu Met Thr Val Ser Leu  
 430 435 440 445

TCC CTG CCA AGT GAT TCT AGC ATG TTC AAC AAT AAC CGC TCC TCA TCA  
 1752

Ser Leu Pro Ser Asp Ser Ser Met Phe Asn Asn Asn Arg Ser Ser Ser  
 450 455 460

CCT AGT GAA CAA GGG TCC AAC TCG ACT TAC GAT CGC ATC TTT CCC CTT  
 1800

Pro Ser Glu Gln Gly Ser Asn Ser Thr Tyr Asp Arg Ile Phe Pro Leu  
 465 470 475

CGC CCT GAC TAC CAG GAG CCA TCC AGG CTG ATA CGA AAA CTC CCA GAA  
 1848

Arg Pro Asp Tyr Gln Glu Pro Ser Arg Leu Ile Arg Lys Leu Pro Glu  
 480 485 490

TTT GCT CCA GGG GAG GAG TCA GGC TGC AGC GGT GTT GTG AAG CCA  
 1896

Phe Ala Pro Gly Glu Glu Ser Gly Cys Ser Gly Val Val Lys Pro  
 495 500 505

GTC CAG CCC AGT GGC CCT GAG GGG GTG CCC CAC TAT GCA GAG GCT GAC  
 1944

Val Gln Pro Ser Gly Pro Glu Gly Val Pro His Tyr Ala Glu Ala Asp  
 510 515 520 525

ATA GTG AAC CTC CAA GGA GTG ACA GGA GGC AAC ACA TAC TCA GTG CCT  
 1992

Ile Val Asn Leu Gln Gly Val Thr Gly Gly Asn Thr Tyr Ser Val Pro  
 530 535 540

GCC GTC ACC ATG GAC CTG CTC TCA GGA AAA GAT GTG GCT GTG GAG GAG  
 2040

Ala Val Thr Met Asp Leu Leu Ser Gly Lys Asp Val Ala Val Glu Glu  
 545 550 555

TTC CCC AGG AAA CTC CTA ACT TTC AAA GAG AAG CTG GGA GAA GGA CAG  
2088  
 Phe Pro Arg Lys Leu Leu Thr Phe Lys Glu Lys Leu Gly Glu Gly Gln  
 560 565 570

TTT GGG GAG GTT CAT CTC TGT GAA GTG GAG GGA ATG GAA AAA TTC AAA  
2136  
 Phe Gly Glu Val His Leu Cys Glu Val Glu Gly Met Glu Lys Phe Lys  
 575 580 585

GAC AAA GAT TTT GCC CTA GAT GTC AGT GCC AAC CAG CCT GTC CTG GTG  
2184  
 Asp Lys Asp Phe Ala Leu Asp Val Ser Ala Asn Gln Pro Val Leu Val  
 590 595 600 605

GCT GTG AAA ATG CTC CGA GCA GAT GCC AAC AAG AAT GCC AGG AAT GAT  
2232  
 Ala Val Lys Met Leu Arg Ala Asp Ala Asn Lys Asn Ala Arg Asn Asp  
 610 615 620

TTT CTT AAG GAG ATA AAG ATC ATG TCT CGG CTC AAG GAC CCA AAC ATC  
2280  
 Phe Leu Lys Glu Ile Lys Ile Met Ser Arg Leu Lys Asp Pro Asn Ile  
 625 630 635

ATC CAT CTA TTA TCT GTG TGT ATC ACT GAT GAC CCT CTC TGT ATG ATC  
2328  
 Ile His Leu Leu Ser Val Cys Ile Thr Asp Asp Pro Leu Cys Met Ile  
 640 645 650

ACT GAA TAC ATG GAG AAT GGA GAT CTC AAT CAG TTT CTT TCC CGC CAC  
2376  
 Thr Glu Tyr Met Glu Asn Gly Asp Leu Asn Gln Phe Leu Ser Arg His  
 655 660 665

GAG CCC CCT AAT TCT TCC TCC AGC GAT GTA CGC ACT GTC AGT TAC ACC  
2424  
 Glu Pro Pro Asn Ser Ser Ser Asp Val Arg Thr Val Ser Tyr Thr  
 670 675 680 685

AAT CTG AAG TTT ATG GCT ACC CAA ATT GCC TCT GGC ATG AAG TAC CTT  
2472  
 Asn Leu Lys Phe Met Ala Thr Gln Ile Ala Ser Gly Met Lys Tyr Leu  
 690 695 700

TCC TCT CTT AAT TTT GTT CAC CGA GAT CTG GCC ACA CGA AAC TGT TTA  
2520  
 Ser Ser Leu Asn Phe Val His Arg Asp Leu Ala Thr Arg Asn Cys Leu

705

710

715

GTG GGT AAG AAC TAC ACA ATC AAG ATA GCT GAC TTT GGA ATG AGC AGG  
 2568

Val Gly Lys Asn Tyr Thr Ile Lys Ile Ala Asp Phe Gly Met Ser Arg  
 720 725 730

AAC CTG TAC AGT GGT GAC TAT TAC CGG ATC CAG GGC CGG GCA GTG CTC  
 2616

Asn Leu Tyr Ser Gly Asp Tyr Tyr Arg Ile Gln Gly Arg Ala Val Leu  
 735 740 745

CCT ATC CGC TGG ATG TCT TGG GAG AGT ATC TTG CTG GGC AAG TTC ACT  
 2664

Pro Ile Arg Trp Met Ser Trp Glu Ser Ile Leu Leu Gly Lys Phe Thr  
 750 755 760 765

ACA GCA AGT GAT GTG TGG GCC TTT GGG GTT ACT TTG TGG GAG ACT TTC  
 2712

Thr Ala Ser Asp Val Trp Ala Phe Gly Val Thr Leu Trp Glu Thr Phe  
 770 775 780

ACC TTT TGT CAA GAA CAG CCC TAT TCC CAG CTG TCA GAT GAA CAG GTT  
 2760

Thr Phe Cys Gln Glu Gln Pro Tyr Ser Gln Leu Ser Asp Glu Gln Val  
 785 790 795

ATT GAG AAT ACT GGA GAG TTC TTC CGA GAC CAA GGG AGG CAG ACT TAC  
 2808

Ile Glu Asn Thr Gly Glu Phe Phe Arg Asp Gln Gly Arg Gln Thr Tyr  
 800 805 810

CTC CCT CAA CCA GCC ATT TGT CCT GAC TCT GTG TAT AAG CTG ATG CTC  
 2856

Leu Pro Gln Pro Ala Ile Cys Pro Asp Ser Val Tyr Lys Leu Met Leu  
 815 820 825

AGC TGC TGG AGA AGA GAT ACG AAG AAC CGT CCC TCA TTC CAA GAA ATC  
 2904

Ser Cys Trp Arg Arg Asp Thr Lys Asn Arg Pro Ser Phe Gln Glu Ile  
 830 835 840 845

CAC CTT CTG CTC CTT CAA CAA GGC GAC GAG TGATGCTGTC AGTGCCTGGC  
 2954

His Leu Leu Leu Leu Gln Gln Gly Asp Glu  
 850 855

CATGTTCTTA CGGCTCAGGT CCTCCCTACA AGACCTACCA CTCACCCATG CCTATGCCAC

3014

TCCATCTGGA CATTAAATGA AACTGAGAGA CAGAGGCTTG TTTGCTTGC CCTCTTTCC  
3074

TGGTCACCCC CACTCCCTAC CCCTGACTCA TATATACTTT TTTTTTTAC ATTAAAGAAC  
3134

TAAAAAAA AAAAAG GCG  
3157

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 855 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ile	Leu	Ile	Pro	Arg	Met	Leu	Leu	Val	Leu	Phe	Leu	Leu	Leu	Pro
1						5					10				15

Ile	Leu	Ser	Ser	Ala	Lys	Ala	Gln	Val	Asn	Pro	Ala	Ile	Cys	Arg	Tyr
								25					30		

Pro	Leu	Gly	Met	Ser	Gly	Gly	Gln	Ile	Pro	Asp	Glu	Asp	Ile	Thr	Ala
								35		40			45		

Ser	Ser	Gln	Trp	Ser	Glu	Ser	Thr	Ala	Ala	Lys	Tyr	Gly	Arg	Leu	Asp
								50		55		60			

Ser	Glu	Glu	Gly	Asp	Gly	Ala	Trp	Cys	Pro	Glu	Ile	Pro	Val	Glu	Pro
								65		70		75		80	

Asp	Asp	Leu	Lys	Glu	Phe	Leu	Gln	Ile	Asp	Leu	His	Thr	Leu	His	Phe
								85		90		95			

Ile	Thr	Leu	Val	Gly	Thr	Gln	Gly	Arg	His	Ala	Gly	Gly	His	Gly	Ile
								100		105		110			

Glu	Phe	Ala	Pro	Met	Tyr	Lys	Ile	Asn	Tyr	Ser	Arg	Asp	Gly	Thr	Arg
								115		120		125			

Trp Ile Ser Trp Arg Asn Arg His Gly Lys Gln Val Leu Asp Gly Asn

130	135	140													
Ser	Asn	Pro	Tyr	Asp	Ile	Phe	Leu	Lys	Asp	Leu	Glu	Pro	Pro	Ile	Val
145						150				155					160
Ala	Arg	Phe	Val	Arg	Phe	Ile	Pro	Val	Thr	Asp	His	Ser	Met	Asn	Val
						165			170					175	
Cys	Met	Arg	Val	Glu	Leu	Tyr	Gly	Cys	Val	Trp	Leu	Asp	Gly	Leu	Val
				180				185					190		
Ser	Tyr	Asn	Ala	Pro	Ala	Gly	Gln	Gln	Phe	Val	Leu	Pro	Gly	Gly	Ser
				195			200					205			
Ile	Ile	Tyr	Leu	Asn	Asp	Ser	Val	Tyr	Asp	Gly	Ala	Val	Gly	Tyr	Ser
				210			215				220				
Met	Thr	Glu	Gly	Leu	Gly	Gln	Leu	Thr	Asp	Gly	Val	Ser	Gly	Leu	Asp
				225			230			235				240	
Asp	Phe	Thr	Gln	Thr	His	Glu	Tyr	His	Val	Trp	Pro	Gly	Tyr	Asp	Tyr
				245				250				255			
Val	Gly	Trp	Arg	Asn	Glu	Ser	Ala	Thr	Asn	Gly	Tyr	Ile	Glu	Ile	Met
				260				265				270			
Phe	Glu	Phe	Asp	Arg	Ile	Arg	Asn	Phe	Thr	Thr	Met	Lys	Val	His	Cys
				275			280				285				
Asn	Asn	Met	Phe	Ala	Lys	Gly	Val	Lys	Ile	Phe	Lys	Glu	Val	Gln	Cys
				290			295				300				
Tyr	Phe	Arg	Ser	Glu	Ala	Ser	Glu	Trp	Glu	Pro	Asn	Ala	Ile	Ser	Phe
				305			310			315			320		
Pro	Leu	Val	Leu	Asp	Asp	Val	Asn	Pro	Ser	Ala	Arg	Phe	Val	Thr	Val
				325				330				335			
Pro	Leu	His	His	Arg	Met	Ala	Ser	Ala	Ile	Lys	Cys	Gln	Tyr	His	Phe
				340				345				350			
Ala	Asp	Thr	Trp	Met	Met	Phe	Ser	Glu	Ile	Thr	Phe	Gln	Ser	Asp	Ala
				355			360				365				
Ala	Met	Tyr	Asn	Asn	Ser	Glu	Ala	Leu	Pro	Thr	Ser	Pro	Met	Ala	Pro
				370			375				380				
Thr	Thr	Tyr	Asp	Pro	Met	Leu	Lys	Val	Asp	Asp	Ser	Asn	Thr	Arg	Ile

385	390	395	400
Leu Ile Gly Cys Leu Val Ala Ile Ile Phe Ile	Leu Leu Ala Ile Ile		
405	410		415
Val Ile Ile Leu Trp Arg Gln Phe Trp Gln Lys Met	Leu Glu Lys Ala		
420	425		430
Ser Arg Arg Met Leu Asp Asp Glu Met Thr Val Ser	Leu Ser Leu Pro		
435	440		445
Ser Asp Ser Ser Met Phe Asn Asn Asn Arg Ser Ser	Pro Ser Glu		
450	455		460
Gln Gly Ser Asn Ser Thr Tyr Asp Arg Ile Phe Pro	Leu Arg Pro Asp		
465	470		480
Tyr Gln Glu Pro Ser Arg Leu Ile Arg Lys Leu Pro	Glu Phe Ala Pro		
485	490		495
Gly Glu Glu Glu Ser Gly Cys Ser Gly Val Val Lys	Pro Val Gln Pro		
500	505		510
Ser Gly Pro Glu Gly Val Pro His Tyr Ala Glu Ala	Asp Ile Val Asn		
515	520		525
Leu Gln Gly Val Thr Gly Gly Asn Thr Tyr Ser Val	Pro Ala Val Thr		
530	535		540
Met Asp Leu Leu Ser Gly Lys Asp Val Ala Val	Glu Glu Phe Pro Arg		
545	550		560
Lys Leu Leu Thr Phe Lys Glu Lys Leu Gly Glu Gly	Gln Phe Gly Glu		
565	570		575
Val His Leu Cys Glu Val Glu Gly Met Glu Lys Phe	Lys Asp Lys Asp		
580	585		590
Phe Ala Leu Asp Val Ser Ala Asn Gln Pro Val	Leu Val Ala Val Lys		
595	600		605
Met Leu Arg Ala Asp Ala Asn Lys Asn Ala Arg	Asn Asp Phe Leu Lys		
610	615		620
Glu Ile Lys Ile Met Ser Arg Leu Lys Asp Pro	Asn Ile Ile His Leu		
625	630		640
Leu Ser Val Cys Ile Thr Asp Asp Pro Leu Cys Met	Ile Thr Glu Tyr		

	645	650	655
Met Glu Asn Gly Asp Leu Asn Gln Phe Leu Ser Arg His Glu Pro Pro			
660	665		670
Asn Ser Ser Ser Asp Val Arg Thr Val Ser Tyr Thr Asn Leu Lys			
675	680		685
Phe Met Ala Thr Gln Ile Ala Ser Gly Met Lys Tyr Leu Ser Ser Leu			
690	695	700	
Asn Phe Val His Arg Asp Leu Ala Thr Arg Asn Cys Leu Val Gly Lys			
705	710	715	720
Asn Tyr Thr Ile Lys Ile Ala Asp Phe Gly Met Ser Arg Asn Leu Tyr			
725	730		735
Ser Gly Asp Tyr Tyr Arg Ile Gln Gly Arg Ala Val Leu Pro Ile Arg			
740	745		750
Trp Met Ser Trp Glu Ser Ile Leu Leu Gly Lys Phe Thr Thr Ala Ser			
755	760	765	
Asp Val Trp Ala Phe Gly Val Thr Leu Trp Glu Thr Phe Thr Phe Cys			
770	775	780	
Gln Glu Gln Pro Tyr Ser Gln Leu Ser Asp Glu Gln Val Ile Glu Asn			
785	790	795	800
Thr Gly Glu Phe Phe Arg Asp Gln Gly Arg Gln Thr Tyr Leu Pro Gln			
805	810		815
Pro Ala Ile Cys Pro Asp Ser Val Tyr Lys Leu Met Leu Ser Cys Trp			
820	825		830
Arg Arg Asp Thr Lys Asn Arg Pro Ser Phe Gln Glu Ile His Leu Leu			
835	840	845	
Leu Leu Gln Gln Gly Asp Glu			
850	855		

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "Ala can be exchanged for any amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asn Pro Ala Tyr  
1

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Thr Tyr Ala Xaa Pro Xaa Xaa Xaa Pro Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

His Arg Asp Leu Ala Ala

1

5

## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGAATTCCCA YMGNRAYYTN RCNRCNMG  
28

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /note= "Xaa can be either Phe or Tyr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ser Asp Val Trp Ser Xaa  
1 5

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGAATTCCYW YNSWGGTNTG SAGNST  
26

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

His Phe Asp Pro Ala Lys Asp Cys Arg Tyr Ala Leu Gly Met Gln A  
sp 1 5 10 15

Arg Thr Ile

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

eu Arg Pro Pro Phe Ser Gln Leu His Arg Phe Leu Ala Glu Asp Ala L  
 1 5 10 15

Asn Thr Val

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Pro Ala Met Ala Trp Glu Gly Glu Pro Met Arg His Asn Leu  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

is Cys Trp Ser Arg Glu Ser Glu Gln Arg Pro Pro Phe Ser Gln Leu H  
 1 5 10 15

Arg